

How to interpret longer than expected match lists

Introduction

In the legacy version of Search & Match Service, search coordinators were limited and could see 2,000 results potential matches when they initiated a search. Following popular demand, WMDA makes it possible to view ALL potential stem cell sources when a search is initiated with the added relief of pagination to allow your browser to load the results faster.

WMDA has received feedback from search coordinators who are receiving an overwhelming number of potential matches and find it difficult to identify the most relevant stem cell source for their patient. It is important to make a distinction between "relevant" and "suitable" when it comes to donor search. While the algorithm returns all possible potentially matched stem cells sources, you would like to view the most relevant stem cell sources toward the top of the match list based on their probability to be HLA-matched for your patient. However, match grade might not always be the only parameter for donor selection and thus donor suitability based on non-HLA factors and the patient's clinical status should also be considered.

The more variability (HLA mismatches, considered loci or untyped loci) you allow in your search, the more potential donors and/or cord blood units will be returned by the algorithm. You might also notice results being returned that seem to be an obvious mismatch.

This most commonly occurs when the patient is homozygous at one or more loci and the typing for the donor contains a null allele.

Since a homozygous typing is generally considered a match with a donor that has one allele that matches the homozygous patient typing and the other is a null allele, Hap-E returns this donor/cord blood unit as a potential match.

Please see the slide below from a recent webinar:

1. Null allele treatment in Hap-E search

- Null alleles are treated as absent, i.e. the second typing matches as homozygous.
- Null allele matching rules are applied to:
 - All high resolution null alleles.
 - Null alleles as part of multi allele codes if the null allele is part of a haplotype matching the donor's (patient's) HLA typing.
- Null allele matching rules are only applied to one typing of the locus.

02:GFJM \triangleq 02:01/02:105/02:125N

Patient typing		Donor typing
A*03:01, A*01:11N	matches	A*03:01, A*03:01
A*03:01, A*01:11N	matches	A*03:01, A*02:125N
If there is a haplotype compatible with the donor typing containing A*02:125N then		
A*03:01, A*01:11N	matches	A*03:01, A*02:GFJM
A*03:01, A*03:01	matches	A*03:01, A*02:XX
A*03:01, A*03:01	does not match	A*03:01, A*01:01:01G
A*01:11N, A*02:125N	does not match	A*03:01, A*03:01

Tips to reduce the number of options on your match list - search coordinators in the driving seat

The way those results are originally sorted in the browser is determined by WMDA, not the algorithm, and can be adjusted by search coordinators to sort the results they deem to be relevant or on a case by case basis. Please keep in mind that an algorithm designed for probability matching will just calculate "chances" and you should use it as a tool in combination with your own knowledge of HLA and the transplant centre's (TC) preferences for the patient. Do not select donors/cord blood units solely on the probabilities calculated by the system. You can read more about haplotype frequencies [here](#).

Steps you can take to ensure the most relevant donors are identified:

Step 1: Ensure that the filter to display donors typed for HLA-DRB1 is selected

In the legacy system when running a standard donor search, all returned donors have values for HLA-A, -B and -DRB1. This is different when running a search in the new system. There all donors need to have typing at HLA-A, -B and at least one other locus (which may or may not be HLA-DRB1). This means that donors and/or cord blood units are shown on the match list that do not have typing at HLA-DRB1. This typically explains the majority of the difference in number of search results as mentioned in the search summary. Although in some cases these donors with typing at HLA-A, -B and -C or -DQB1 may prove useful, in most cases they are not. We therefore apply a default filter to all search results.

You can see all donors by unchecking the default filter.

Donor

☒ Return only records with DRB1

Step 2: Sort mismatch results by "Sum of probabilities"

This format of group/sorting is not considered a filter as all the results are still displayed, but just in a different order. You might find many irrelevant potential fully matched results but find that they all have a low overall match probability for P0. When performing a 1 mismatch search and applying the "sum of probabilities" sorting method, the values for P0 and P1 are summed and the highest probability donors are then displayed toward the top of the page. When performing a 2 mismatch search and applying the "sum of probabilities" sorting method, the values for P0, P1 and P2 are added and the highest probability donors are then displayed toward the top of the page.

Filters

Match

Locus mismatch allowed

Select loci



DPB1 match grade

Select match grade



Grouping/Sorting



☒ Standard

☐ Sort by sum of probabilities

Step 3: Make use of HLA filters

When performing a mismatch search, the transplant centre might have some preferences on where said mismatch should or should not be. You can filter for this in the updated Search & Match Service to ensure that the most relevant and/or suitable results appear on the list.

Filters

Match

Locus mismatch allowed

Select loci



Step 4: Make use of other non-HLA filters

Several other filters have been implemented to reduce the list of results even more. When applying these filters, it is however important to note that the results that do not meet the selected criteria are filtered from the list and no longer displayed by the browser. This means that by over filtering you could possibly miss the most relevant and/or suitable match for your patient. Filters include: DPB1 match grade, CMV, sex, blood group and registry. Secondary sorting and overall filtering for both TNC and CD34+ is also available for cord blood searches.

Step 5: Search Advisory

If you are experiencing difficulties in your selection of a donor/cord for your patient, you can request a search advice from the WMDA HLA experts. To request an advise, go to your patient list, click on the patient ID and at the bottom of the Update patient form you will find a button with 'Request Search Advisory'. An email message will then open with the patient information and some additional fields with requirements. Please fill out as much as possible and send the email. You will receive the advice also by email.